



MAQC2026

Precision in a Complex World

**22-26 SEPTEMBER 2026
BRESCIA, ITALY**

FULL PROGRAM

MAQC Society 2026 Annual Meeting

Co-organized by the International Human Phenome Institute (IHPI), Shanghai

Under the Patronage of University of Brescia

Sponsored by Bristol Myers Squibb | JMP Statistical Discovery

LIGHT | University of Brescia | MAQC Society

<https://themaqc.org/conferences/>

Conference overview

MAQC2026 brings together international academic, regulatory, clinical and industry communities to advance reproducibility, quality, benchmarking and trustworthy translation across artificial intelligence, omics and complex health data.

The four-day program combines a pre-conference, technical tutorials, parallel activities with the International Human Phenome Institute (IHPI), two main conference days, selected abstracts, posters and community-led planning for the next generation of MAQC studies. A post-conference workshop day on future MAQC Initiatives closes the program.

Program at a glance

Date	Program	
Tue 22 Sept	Special Pre-conference Program	IHPI Workshop Day 1
Wed 23 Sept	Technical Tutorials and Community Meetings	IHPI Workshop Day 2
Thu 24 Sept	Main Conference Day 1	
Fri 25 Sept	Main Conference Day 2	
Sat 26 Sept	Future MAQC Initiatives Workshop, by arrangement	

Participation

- Registration is open.
- **Abstract submission is open for posters until Sept 4** - a selection of accepted posters will be additionally offered a short talk.
- Abstracts should be under 400 words. A free EasyChair user ID is required if you do not already have one.

Program updates, registration and abstract submission: <https://themaqc.org/conferences/>

Venue

- CSMT Center Brescia (Sept, 22-23) - Via Branze 45, 25123 Brescia
- Engineering Department (Sept, 24-25) - University of Brescia, North Campus, Via Branze 38, 25123 Brescia, Italy

All times are in Central European Summer Time (CEST, GMT+2).

PRE-CONFERENCE DAY 1

Tue 22 Sept

SPECIAL PRE-CONFERENCE PROGRAM DAY PARALLEL SESSIONS 1 & 2	MAQC: The Future of Clinical Practice, Drug Discovery, and Regulatory Science in the AI Era	IHPI - Building the Future of Human Phenomics (Day 1), <i>organized by the International Human Phenome Institutes (IHPI), Shanghai.</i>
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Parallel Session 1 - The Future of Clinical Practice, Drug Discovery, and Regulatory Science in the AI Era: a MAQC seminar day for researchers and industry professionals.

09:30-13:00	P01 DIGITAL TWINS AND REGULATORY REPRODUCIBILITY <i>Invited talks and discussion</i>
FOCUS	Digital twins for clinical trials, translational decision-making, regulatory reproducibility and trustworthy AI, digital biomarkers
Viswanath Devanarayan	Digital twins for clinical trial efficiency: patient enrichment, synthetic controls, and prognostic covariates
Daniela Seneca	Gaps & Practical Challenges on Medical Device Artificial Intelligence conformity assessment: Perspectives from a Notified Body
Break	
Weida Tong	50 Shades of AI in Regulatory Science
Emanuela Oldoni	Digital and phenotypic biomarkers: an EU regulatory and data perspective
Lunch	

14:00-15:00	P02 AI Drug Discovery <i>Invited talks and discussion</i>
FOCUS	Regulatory sandboxes, certification pathways, and translational validation of AI systems.
Tudor Oprea	Introducing AIDDA, an AI Drug Discovery Agent
Short Break	

15:15-17:15	P03 REGULATORY AI, CLINICAL EVIDENCE, AND REPRODUCIBLE TRANSLATION <i>Panel discussion</i>
FOCUS	A debate on the role of AI in reproducibility across regulatory, clinical, and industry settings. Coordinated by Weida Tong (FDA-NCTR). Emilio Merlo Pich (DIB Bologna), Filippo Lunghini (Dompé), Rebecca Kusko (Cellino Bio), Wendell Jones (IQVIA Laboratories).

Parallel Session 2 – Building the Future of Human Phenomics - Day 1

09:30-12:30	P-HP1 Human Phenome Efforts from around the world <i>Invited talks and discussion</i>
FOCUS	Overview of human phenome initiatives from the U.S., China, Europe, and Canada
Lee Hood, CEO, Phenome Health / ISB, Seattle	US Phenome Initiatives
Felix Li JIN, President, Fudan University	Shanghai Phenome Projects
Adil Mardinoglu, King's College London	European and Turkish Phenome Longevity Efforts
Break	
To be defined	Luxembourg/Canadian Phenome Initiatives
Leming Shi, President, IHPI	Multi-omics standardization
Qiang Tian, IHPI	The PhenoQC initiative
Lunch Break	

15:00-17:00	P-HP2 Organizational structures supporting the human phenome efforts <i>Invited talks and discussion</i>
FOCUS	Overview of International Society of Phenomics, Alliance of Open Life Science, and Phenomics and Vita Data
Weishuo Tao	Introduction of the International Society of Phenomics
Bin-Zhi Qian, Fudan Univ	Introduction of the Alliance of Open Life Science
Han Liu	Phenomics and Vita Data: Exploration and Practice of Scholarly Publishing
Short Break	
IHPI Board	Open Discussion: How to Strengthen the Network and Cooperation in the Field of Phenomics

PRE-CONFERENCE DAY 2

Wed 23 Sept

PRE-CONFERENCE PROGRAM DAY	MAQC Technical Tutorial Day	IHPI - Building the Future of Human Phenomics (Day 2), <i>organized by the International Human Phenome Institutes (IHPI), Shanghai.</i>
PARALLEL SESSIONS		

09:30-11:00	P04 AI-ASSISTED WIDE DATA ANALYSIS <i>Technical tutorial</i>
FOCUS	AI-assisted analysis across genomics, clinical, image-derived, and wide biomedical data.
Russ Wolfinger	AI-Assisted Wide Data Analysis: a tutorial This training introduces life scientists to the AI/ML in JMP, enabling predictive modeling with tabular data, images, and text. Participants will learn how to leverage pretrained deep learning models, fine-tune models for their own data, and build classification and regression models while interactively assessing, comparing, and interpreting model performance, all without writing code.
Break	

11:30-13:00	P05 TOOLS FOR REAL-WORLD EVIDENCE AND FEDERATED DATA <i>Technical tutorial</i>
FOCUS	OMOP, federated data, EHDS, 1M+ Genomes, and European health data communities.
Giovanni Tonon Michela Riba	The tutorial will describe tools and standards for RWE and Federated data developed and applied in a large-scale collaborative experience.
Lunch	

14:00-15:30	P06 PUBLISHING REUSABLE AI/ML MODELS IN THE LIFE SCIENCES <i>Technical tutorial</i>
FOCUS	ELIXIR ecosystem, DOME, OSAI.
Gavin Farrell	Publishing Reusable AI/ML Models in the Life Sciences This tutorial introduces practical frameworks for developing, documenting, publishing, and reusing AI/ML models in the life sciences. Participants will learn how the DOME and OSAI frameworks support transparent model reporting, validation, and reuse, with examples from the ELIXIR ecosystem and hands-on discussion of emerging tools such as the DOME registry and DOME copilot
Break	

16:00-17:30	P07 SPATIAL TRANSCRIPTOMICS TUTORIAL <i>Technical tutorial</i>
FOCUS	Spatial transcriptomics methods and analysis for omics and image-derived data.
Carissa Chen	Spatial transcriptomics Tutorial: from raw spatial data to generating biological insights. Spatial transcriptomics introduces exciting opportunities and analytical challenges to investigate how tissue architecture and extracellular signaling within the microenvironment shape cellular identity and function across development, health, and disease. The multiple data modalities - spatial coordinates, images and gene expression introduces greater potential to interrogate advanced biological hypotheses. However, the added complexity also introduces technology-specific biases and artifacts, together with important considerations during experimental design. In this tutorial, we will cover biases associated with spatial transcriptomics platforms and discuss key considerations for designing 'good' spatial experiments. Participants will examine essential processing and quality-control measures for image-based spatial transcriptomics. Then, we will introduce analytical approaches for investigating the tissue microenvironment, focusing on cellular neighbourhoods, spatial co-localisation, and interactions among cell types and tissue structures. By the end of the workshop, participants will be equipped to make informed decisions about experimental design, and an understanding of emerging areas in spatially-aware computational method development leveraging bioinformatics and deep learning/foundation model approaches to characterise fundamental biological mechanisms.
Christopher Mason	A short review on spatial omics and imaging technologies

17:30-18:30	P08 ITALIAN SINGLE CELL SPATIAL OMICS CORE CENTERS FORUM <i>Meeting</i>
FOCUS	Italian core center updates and networking on single-cell and spatial omics technologies

Parallel Session 2 – Building the Future of Human Phenomics - Day 2

09:30-12:00	P-HP3 Clinical Translation of Phenomics <i>Invited talks and discussion</i>
CHAIR	Leming Shi, President, International Human Phenome Institutes (Shanghai)
Yan Zheng, Fudan Univ.	Phenomics-Informed Precision Nutrition: Insights from Chinese Cohorts
Bin-Zhi Qian, Fudan Univ.	Unifying Tumor-Associated Macrophage Heterogeneity via Single-Cell and Spatial Omics
Break	

09:30-12:00	P-HP3 Clinical Translation of Phenomics - continued <i>Invited talks and discussion</i>
George Haddad	Beyond SOAP: A Cognitive Framework for Systems and Longevity Medicine
Yibin Feng, HKU	TCM strategy for metabolic diseases and cancer
George Haddad, Yibin Feng, HKU	How to Establish Scientific Wellness Clinics
LUNCH	

MAIN CONFERENCE DAY 1

Thu 24 Sept

09:00-10:00	P09 PRECISION IN A COMPLEX WORLD: JOINT SESSION WITH IHPI <i>Keynote / joint session</i>
FOCUS	Opening joint session and invited lecture connecting MAQC reproducibility, precision medicine, and human phenome-scale science.
MAQC2026 Organizers	MAQC2026: Welcome and useful information
Lee Hood	The International Human Phenome Initiative

10:00-11:10	P10 AI FOR CLINICAL TRIALS <i>Main conference session</i>
FOCUS	AI for clinical trial efficiency, synthetic controls, patient enrichment, and outcome prediction.
Viswanath Devanarayan	Digital twins for clinical-trial efficiency
Wenjun Bao	AI-Enhanced capabilities of clinical trial software broadly used by Industry and Regulatory Agencies
Break	

11:30-13:00	P11 Digital Biomarkers: Ensuring Quality, Reproducibility, and Trust in Personalized Medicine <i>Main conference session</i>
FOCUS	Collaborative benchmarking initiatives, data standards, and best practices can improve the reliability and regulatory acceptance of digital biomarkers.
Emanuela Oldoni, Luca Palmerini, Stefano Sapienza	Regulatory pathways for the validation of digital biomarkers. Critical challenges related to data quality, reproducibility, benchmarking, and validation of Digital biomarkers derived from wearable devices, mobile technologies, and remote monitoring platforms, for their combination with multi-omics, clinical, and real-world datasets .
Lunch	

14:00-14:45	P12 Shaping the future of medicine on Earth and in space. <i>Main conference session</i>
FOCUS	The challenge of extreme operational environments on human biology. HERO builds on the astronaut research established through "From SOMA (Space Omics and Medical Atlas) to HERO" (Humans in Extreme Environments Research Omics)
Christopher Mason	The Bikini Atoll Expedition: testing extreme environments to develop life-sustaining medical technologies for deep space exploration and healthcare on Earth.

14:45-15:30	P13 WHAT IS NEXT FOR COMMUNITY-LED MAQC STUDIES – Part 1 <i>Main conference session</i>
FOCUS	Future community-led MAQC studies, reference materials, reproducible evidence, and collaborative priorities
MAQC Board	Visions for MAQC - Ensuring multi-omics data reproducibility for AI with reference materials as a common calibrator - Developing reference materials & datasets for standardizing multi-omics liquid biopsy

15:30-16:15	P14a SELECTED ABSTRACT HIGHLIGHTS <i>Short talks</i>
FOCUS	Selected abstracts, short oral highlights, from contributions
JangKeun Kim	From Reproducible Pipelines to Reproducible Claims: An Audit of Model Selection and Aggregation in Spaceflight Omics (oral contribution)
Fuyao Li	Single-Cell Transcriptomics Unveils Convergent Microglial Immunometabolic Reprogramming Underlying the Anti-Alzheimer Efficacy of Two Standardized Kidney-Tonifying Formulations (remote oral contribution)
Yu Zhang	A metrological foundation for absolute transcriptomics using International System of Units-anchored calibrators (oral contribution)

16:30-18:30	P14b MAQC2026 POSTER SESSION <i>Poster Session</i>
FOCUS	Contributed posters
Poster	POSTER SESSION – FOYER AREA

MAIN CONFERENCE DAY 2

Fri 25 Sept

9:00-10:20	P15 AI IN DRUG DISCOVERY, TOXICOLOGY, AND SAFETY <i>Community Project Updates</i>
FOCUS	AI for drug discovery, toxicology, safety, regulatory science, pharmacovigilance, and regulatory review.
Weida Tong	From Animals to Algorithms: A Regulatory Science Perspective
Joshua Xu	AI for Pharmacovigilance and Beyond
Wenzhong Xiao	An Agent-Driven, Self-Evolving AI Platform for Disease Research and Drug Discovery

10:20-11:25	P16 SCALING UP FOR A GLOBAL DATA VISION <i>Main conference session</i>
FOCUS	EHDS national cancer data nodes, interoperability, standards, data quality, and trustworthy real-world evidence.
Giovanni Tonon	Cancer Minimal Data Sets and Semantics
Lifang Liu	Understanding EHDS. How cancer data node will facilitate trustworthiness of clinical real world health data algorithm development in an AI world. Importance and adoption of data standards, interoperability, data quality, and tools. How EHDS shifts the play of regulatory approval towards real-world evidence-based approach. EHDS and its impact on HTA procedures/national reimbursement.
Break	

11:45-13:00	P17 REPRODUCIBILITY <i>Main conference session and selected submissions</i>
Joaquín Dopazo	Can Synthetic Patients Replace Real Ones? A Million-Scale Diabetes Study
Pawel Labaj	Integrating cross-platform metagenomics studies – high taxonomic concordance and functional analysis challenges
Benjamin Haibe-Kains	ML-ready datasets for AI-driven small molecule discovery

Lunch	
14:00-16:00	P18 COMMUNITY-LED MAQC STUDIES: CLINICAL-GRADE AI/ML-BASED BIOMARKERS (MAQC-ML WG) AND WHAT IS NEXT <i>Technical presentation and community project updates</i>
FOCUS	MAQC-ML results, CML paper update, and recommendations for clinical-grade AI/ML biomarkers. Future community-led MAQC studies, reference materials, reproducible evidence, and collaborative priorities.
Wendell Jones, Russ Wolfinger & the MAQC/ML Working Group	Best Practices for Machine Learning-based Biomarker: Development from a Large Community Challenge Benchmark
David P Kreil	Metric effects on precision in the comparative assessment of machine learning in two large electronic health record cohorts
Wendell Jones & the MAQC Board	Current and future Community-led MAQC studies - The Challenges of Agentic AI in Tumor Boards (B. Haibe-Kains) - Other selected topics
Break	

16:30-17:30	P19 MAQC WORKING GROUPS, 2027-2030 INITIATIVES, PRIZES, AND CLOSING <i>Governance / prizes / closing</i>
FOCUS	Future MAQC actions, prizes, and closing remarks.
Wendell Jones, PhD and MAQC leadership	Future initiatives, prizes and closing

MAQC2027 AND BEYOND

Sat 26 Sept

By arrangement	P20 FUTURE MAQC INITIATIVES WORKSHOP <i>Community / board workshop</i>
FOCUS	Optional community and board-oriented workshop on future MAQC initiatives in the age of AI.
MAQC Board and invited participants	Future MAQC initiatives workshop

Confirmed speakers (selected)



Viswanath Devanarayan, PhD

Bristol Myers Squibb (BMS)



Tudor I. Oprea, MD, PhD

Dompé farmaceutici



Weida Tong, PhD

FDA/NCTR, Division of Bioinformatics and Biostatistics



Joshua Xu, PhD

FDA/NCTR, Division of Bioinformatics and Biostatistics



Emanuela Oldoni

EATRIS EU Working Group on Digital Biomarkers



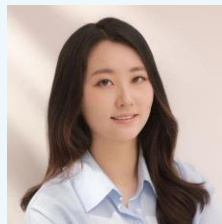
Russ Wolfinger, PhD

JMP



Gavin Farrell

University of Padua



Carissa Chen

University of Padua



Christopher Mason, PhD

Weill Cornell Medicine



Luca Palmerini

University of Bologna



Lee Hood

Phenome Health



Leming Shi

Fudan University

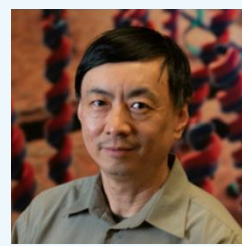
Confirmed speakers (continued)



Wendell Jones, PhD
IQVIA Laboratories; MAQC Society



Wenjun Bao
JMP Statistical Discovery



Wenzhong Xiao
Harvard University



Joaquín Dopazo
Health AI and Data
Barcelonaβeta



Pawel Labaj
Małopolska Centre of Biotechnology,
Jagiellonian University, Poland



Benjamin Haibe-Kains, PhD
University of Toronto /
Princess Margaret Cancer Centre



David Kreil
Boku University, Wien



Giovanni Tonon
Vita-Salute San Raffaele University
Milan (IT)



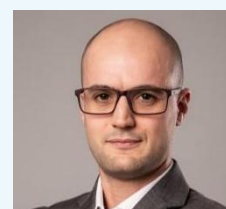
Emilio Merlo Pich
Gelf Health; OMEXIA;
IFAB Foundation



Stefano Sapienza
Centre for Systems Biomedicine
(LCSB), Luxembourg



Daniela Seneca
BSI Group Italia, Italy



Filippo Lunghini
Dompé farmaceutici

Speaker biographies (selected)



Viswanath Devanarayan, PhD

Bristol Myers Squibb (BMS)

A biostatistics and biomarker-development leader working at the interface of drug development, translational science and clinical evidence. His MAQC2026 contribution focuses on digital twins for clinical-trial efficiency, including patient enrichment, synthetic controls and prognostic covariates.



Tudor I. Oprea

Dompé farmaceutici

Chief AI Drug Discovery Officer at Dompé farmaceutici. He is a digital drug hunter specializing in agentic AI drug discovery and knowledge management for target and drug discovery. Three drugs he co-invented have reached clinical trials, including LNS8801, a GPER agonist in Phase 2/3 for uveal melanoma. He developed DrugCentral and Pharos, two widely used digital resources for drug discovery. He is the recipient of the Hansch Award (2002) and the Fujita Award (2026). He co-authored 13 issued US patents and over 400 peer-reviewed publications.



Weida Tong, PhD

FDA/NCTR, Division of Bioinformatics and Biostatistics

Director of the Division of Bioinformatics and Biostatistics at the FDA National Center for Toxicological Research. His research spans bioinformatics, artificial intelligence, molecular modelling, biomarker discovery, drug safety, toxicogenomics and precision medicine. He has held long-standing leadership roles in MAQC community projects.



Daniela Seneca, PhD

BSI Group Italia, Regulatory Lead, Artificial Intelligence

Biomedical engineer with over 20 years of experience in medical devices on technology transfer, product development, patents, prototyping, technical tests, clinical studies, regulatory affairs and Health Technology Assessment. She worked as lead auditor/medical device expert for the Italian Ministry of Health in the European Commission working groups and Joint Assessments. Currently Regulatory Lead in BSI, responsible for regulatory strategy, policies, procedures and accreditation/designation as a Conformity Assessment Body and Notified Body, after 5 years as technical specialist, clinical team leader and scheme manager for active medical devices, including Artificial Intelligence software. She is a former IEEE member now participating to the CEN-CENELEC Joint Technical Committee 21 on Artificial Intelligence.



Joshua Xu

FDA/NCTR, Division of Bioinformatics and Biostatistics

Dr. Joshua Xu is currently a Senior Biomedical Research and Biomedical Product Assessment Service (SBRBPAS) Expert and the Branch Chief for Research-to-Review and Return (R2R) in the Division of Bioinformatics and Biostatistics at US FDA's National Center for Toxicological Research. His research focused on benchmarking emerging genomics technologies for precision medicine, image analysis for digital pathology and food contamination detection, and adapting AI for regulatory documents review. He oversees the R2R program to translate regulatory science research findings and integrate them with advanced AI technologies into regulatory applications. He is also the Executive Secretary for the MAQC Society.



Emanuela Oldoni

EATRIS Scientific Lead

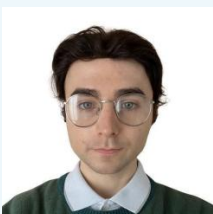
Scientific Lead for Personalised Medicine at EATRIS and coordinator of its Biomarkers Platform. She works across European academic and clinical centres to advance discovery, analytical validation and clinical qualification of molecular and digital biomarkers, supporting patient stratification and translational research. She holds a PhD in Molecular and Translational Medicine.



Russ Wolfinger

JMP Statistical Discovery

Russ Wolfinger is the Director of Scientific Discovery and Genomics at JMP Statistical Software, a SAS company specializing in interactive desktop software for dynamic data visualization and analysis. In this role, Wolfinger leads a team in research and development of JMP software solutions for the life sciences. He joined SAS in 1989 after earning a PhD. in statistics from North Carolina State University. For 10 years, he devoted his efforts to developing and promoting statistical procedures for mixed models and multiple testing. In 2000 he started the Scientific Discovery department at SAS and JMP. Wolfinger is co-author of more than 150 publications and four books; he is the most cited author at SAS. He is a fellow of both the American Association for the Advancement of Science and the American Statistical Association, an adjunct faculty member at North Carolina State University and the University of North Carolina at Chapel Hill, and a Kaggle Competition Grandmaster.



Gavin Farrell

University of Padua

A researcher and trainer working on transparent, reusable AI/ML models in the life sciences. His tutorial introduces practical use of the DOME and OSAI frameworks, model documentation and emerging resources supporting reproducible publication and reuse.



Carissa Chen

University of Padua

A researcher at the University of Padua working on the ERC-funded SPECOLA project, Spatial Transcriptomics through the Lenses of Statistical Modeling and AI. Her work addresses statistical and reproducible analysis of spatially resolved biological data. At MAQC2026 she will introduce methods and practical choices for spatial omics studies.



Christopher Mason

Weill Cornell Medicine

A professor and genomics researcher at Weill Cornell Medicine whose work spans sequencing technologies, single-cell and spatial omics, computational biology and biomedical applications of large-scale molecular data. He serves as Chief Science Advisor to the MAQC Society.



Wenjun Bao

JMP Statistical Discovery

Wenjun Bao is Chief Scientist and Director of Advanced Analytics R&D in the Life Sciences division of JMP Statistical Discovery, a subsidiary of SAS that provides interactive and highly visual statistical discovery software to scientists and engineers. Bao has extensive experience in the clinical, bioinformatics, biochemistry, and molecular biology fields. She has been a research grant review committee member for NIH since 2005 and research advisor for scientists at numerous universities and government agencies around the world. Bao is also an adjunct professor at Fudan University and a CDISC board member. Prior to joining JMP, Bao was a Research Scientist with the U.S. Environmental Protection Agency and a Research Assistant Professor at Duke University. She holds her PhD. from Oregon Health and Science University.



Lee Hood

Phenome Health

Pioneer of systems biology and P4 Medicine, Dr. Hood has founded multiple biotechnology companies, authored more than 1,000 scientific publications, and helped redefine modern biology. He leads Phenome Health's scientific vision and the development of the Human Phenome Initiative.



Joaquín Dopazo

Health AI and Data Barcelonaβeta

A biomedical data scientist with more than 30 years of experience in computational biology, genomics, clinical data and artificial intelligence. He has led research groups in academia, public health and industry, developing systems-biology and data-science approaches for precision medicine, personalised healthcare and drug discovery.



Pawel Labaj

Małopolska Centre of Biotechnology, Jagiellonian University, Poland

Professor and Deputy Director at the Małopolska Centre of Biotechnology, Jagiellonian University. His research focuses on data science methodologies in transcriptomics and metagenomics to advance precision medicine. A board member of the MetaSUB Consortium and long-standing contributor to US FDA SEQC benchmarking projects, his work emphasizes data quality and reproducibility across complex biomedical datasets. At MAQC2026, he will present on integrating cross-platform metagenomics studies and functional analysis challenges.



Benjamin Haibe-Kains

University of Toronto / Princess Margaret Cancer Centre

Dr. Benjamin Haibe-Kains is a Senior Scientist at the Princess Margaret Cancer Centre (PM), University Health Network, and Associate Professor in the Medical Biophysics department of the University of Toronto. Dr. Haibe-Kains earned his PhD in Bioinformatics at the Université Libre de Bruxelles. Supported by a Fulbright Award, he did his postdoctoral fellowship at the Dana-Farber Cancer Institute and Harvard School of Public Health. Dr. Haibe-Kains' research focuses on the integration of high-throughput data from various sources to simultaneously analyze multiple facets of carcinogenesis. His MAQC2026 contribution focuses on ML-ready datasets for AI-driven small-molecule discovery.



Luca Palmerini

Università di Bologna, Italy

A bioengineer and tenure-track researcher at the University of Bologna. His research applies machine learning, signal processing and statistics to movement analysis, with particular emphasis on wearable-sensor data and digital biomarkers for neurological disease, fall prediction and telerehabilitation.



Stefano Sapienza

Centre for Systems Biomedicine (LCSB), Luxembourg

Postdoctoral researcher in the group of Digital Medicine at University of Luxembourg. His work focuses on the translation of sensor-derived measures into practical tools that can be integrated into routine clinical care. At MAQC2026 he will discuss regulatory pathways for the validation of digital biomarkers.



Emilio Merlo Pich

Gelf Health; OMEXIA; IFAB Foundation

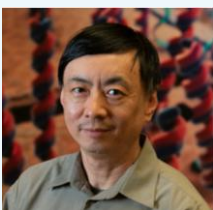
Physician specialising in neurology, Emilio Merlo Pich is CEO of Gelf Health, CMSO of OMEXIA and Senior Advisor to IFAB Foundation. He previously held senior R&D roles at Alfasigma, Takeda, Roche and GSK. His expertise spans drug discovery and clinical development, translational medicine, biomarkers, neuroimaging and digital medicine. His current work focuses on AI applications in medical and pharmaceutical research and preventive precision medicine. He has contributed to European collaborations on digital endpoints and their regulatory qualification. At MAQC2026, he joins the final panel on 22 September, "Regulatory AI, Clinical Evidence, and Reproducible Translation," as an invited contributor.



Leming Shi

Fudan University

A distinguished professor at Fudan University's School of Life Sciences, where he directs centres for pharmacogenomics and clinical genomics. His work focuses on reproducible biomedical big data, biomarker development, pharmacogenomics and precision medicine. He conceived and led the MAQC/SEQC consortia and serves as Chief Science Officer of the MAQC Society.



Wenzhong Xiao

Harvard University
Mass General Research Institute

Dr. Wenzhong Xiao is Director of the Immuno-Metabolic Computational Center at Mass General Hospital (MGH), Harvard Medical School. He also leads a Computational Genomics Group at Stanford Genome Technology Center (SGTC). His research is at the interface of computation, genomics and medicine. A major bottleneck of genome medicine today is around data analysis, interpretation, and integration. His research interest is to develop approaches to address these challenges and to help translate genome technologies to better disease diagnosis, prevention, and therapeutics, especially in studies of human immune and metabolic diseases. In collaboration with research at SGTC and Open Medicine Foundation (OMF), his lab has been analyzing the Severely Ill Patient Big Data Study and other studies on ME / CFS and comparing ME / CFS with other diseases. Dr. Xiao is a member of the OMF Scientific Advisory Board and Co-Director of the OMF funded Harvard ME / CFS Collaboration at the Harvard-Affiliated Hospitals.



David Kreil
Boku University
Wien

David is the WWTF Vienna Science Chair of Bioinformatics at Boku: His interests are: Development of computational and quantitative experimental methods to allow the investigation of complex biological questions that are hard to examine using traditional gene-by-gene approaches alone. Background: System-scale prediction (Scientific Director and Co-Founder, Institute of Advanced Research in Artificial Intelligence), Analysis of life-science data using probabilistic and statistical methods, sequence analysis (Research Fellow of Darwin College and the Medical Research Council UK, Dept of Genetics & Cavendish Laboratory, Univ. of Cambridge). Integration of heterogeneous databases and bioinformatics tools, comparative genome analysis (EMBL fellow, European Bioinformatics Institute, Cambridge). Theory of dynamic properties at phase transitions (Dept of Physics, Technical University of Munich).



Filippo Lunghini
Dompé farmaceutici

Filippo Lunghini, PhD, is a specialist in computational drug discovery, currently Artificial Intelligence Senior Specialist at Dompé farmaceutici, where within the Exscalate ecosystem he drives platform development across the company's core AI research areas — machine learning and predictive modelling, knowledge graphs, and AI Factory — bridging computational research with real-world drug discovery applications. He holds a PhD in Cheminformatics from the University of Strasbourg.



Giovanni Tonon
Vita-Salute San Raffaele University
Milan (IT)

Dr. Giovanni Tonon is full professor, Director of the Center for Omics Sciences, and of the Functional Genomics of Cancer Unit at the University Vita-Salute San Raffaele, in Milan, Italy. After a long stay in the United States, first at the National Cancer Institute, NIH in Bethesda, MD and then as an Instructor in Medicine at the Dana Farber Cancer Institute, Harvard Medical School, Boston, MA, he has joined the San Raffaele Scientific Institute. He is president of DIGICORE, co-coordinates the WG9 of the EU 1+Million Genome initiative, he coordinates the bioinformatics activities of the Italian network Alliance against Cancer (ACC), he co-leads Clinical Informatics group in Digicore and he is in the executive committee of the Health Big Data initiative of the Italian government.



Wendell Jones
IQVIA Laboratories; MAQC Society

Wendell is a consulting statistician and thought leader in industry and is currently Principal Bioinformaticist and Scientific Advisor at IQVIA Laboratories Genomics for the past seven years after leading the genomic bioinformatics organization at EA Genomics for nine years, Wendell has been a part of EA Genomics/Q Squared Solutions/IQVIA Laboratories team for over 20 years and has general interests in bioinformatics, statistical analysis and modeling, statistical graphics, and analyzing large datasets. Wendell has been heavily involved in quality-related consortiums including the Sequencing Quality Control project (SEQC) and the Microarray Quality Control (MAQC) project. Wendell is currently the Executive Chair of the MAQC Society. Wendell's current research interests include sequencing-based studies and clinical applications of RNA, miRNA, and DNA-based biomarkers in addition to other related genomics technologies. At MAQC2026 he will present MAQC-ML work toward clinical-grade AI/ML-based biomarkers.

Join MAQC2026

Registration is open.

Share this program with colleagues working in reproducible science, AI/ML, omics, regulatory science and clinical translation.

<https://themaqc.org/conferences/>

Brescia, Italy | 22-26 September 2026



Program information is subject to refinement. Confirmed speakers are listed as of 08 September 2026.

CONFERENCE ORGANISERS

MAQC Executive Committee

Wendell Jones, PhD, Executive Chair - IQVIA Laboratories (Genomics), USA
 Cesare Furlanello, President - LIGHT Center Brescia & HK3 Lab S.R.L, Italy
 Rebecca Kusko, PhD, Deputy Chair - Cellino Bio, USA
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We sincerely apologize for any typos, errors, or omissions in this conference program.